



# SEQUENCE LISTING

<110> Short, Jay  
Mathur, Eric  
Richardson, Toby  
Robertson, Dan  
Barton, Nelson

<120> Recombinant Phytases and Uses Thereof

<130> 564462010600

<140> US 10/021,723

<141> 2001-12-12

<150> US 60/255,090

<151> 2000-12-12

<160> 74

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1325

<212> DNA

<213> Yersinia pestis

<220>

<221> misc\_feature

<222> 470, 487, 491, 492, 522

<223> n = A, T, C or G

<400> 1

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acgccagata	agtggccaca	atggccggta	aaagcggggt	atttaacgcc	acgtgggtgc	240
gagttgggtca	cattgatggg	ggggttttat	ggtgattact	ttcgcagcct	tggtttggtta	300
gcggcgggat	gtccggcaga	ggggggggta	tatgcacagg	cagatatcga	tcaacgtacc	360
cgcttaaccg	gacaggcatt	tcttgatggg	gtggctccgg	ggtgtgggtt	gaccgtgcat	420
aatcaggccg	atttgaaaaa	gaccgatccc	ctgttccatc	cggtagaggn	tggcgtgtgt	480
aagttanacg	nngcacaaac	agataaaagc	attgaagaac	anttgggcgg	gccgttagat	540
acggtgagcc	agcgctacgc	taaacctttt	gcccagatgg	gggacgtgct	gaattttgcg	600
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cggccaatga	agttaacggt	aataaagaag	ggacaaaagt	gaccctcagt	gggccactgg	720
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tacagcagat	agatacggct	ttaacccttc	aactggatgc	tcaggggcaa	aagctaccca	960
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cgggtatgct	gggagccgac	tggcagctac	ccgagcaacc	tgataatact	ccaccagggtg	1080
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<210> 2

<211> 441  
 <212> PRT  
 <213> Yersinia pestis

<220>  
 <221> VARIANT  
 <222> 157, 163, 164, 174  
 <223> Xaa = Any Amino Acid

<400> 2

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Gly	Tyr	Thr	Leu	Glu	Arg	Val	Val	Ile	Leu	Ser	Arg	His	Gly	Val	Arg
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Lys	Leu	Xaa	Xaa	Ala	Gln	Thr	Asp	Lys	Ala	Ile	Glu	Glu	Xaa	Leu	Gly
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		180					185						190		
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225				230						235					240
Ala	Leu	Ser	Ser	Thr	Leu	Gly	Glu	Ile	Phe	Leu	Leu	Gln	Asn	Ala	Gln
			245					250						255	
Ala	Met	Pro	Glu	Val	Ala	Trp	Gln	Arg	Leu	Lys	Gly	Ala	Glu	Asn	Trp
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Val	Ser	Leu	Leu	Ser	Leu	His	Asn	Ala	Gln	Phe	Asn	Leu	Met	Ala	Lys
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Thr	Pro	Tyr	Ile	Ala	Arg	His	Lys	Gly	Thr	Pro	Leu	Leu	Gln	Gln	Ile
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Ile	Ser	Ala	Gln	Asn	Arg	Val	Leu	Phe	Leu	Gly	Gly	His	Asp	Thr	Asn
			325					330						335	
Ile	Ala	Asn	Ile	Ala	Gly	Met	Leu	Gly	Ala	Asp	Trp	Gln	Leu	Pro	Glu
		340					345						350		
Gln	Pro	Asp	Asn	Thr	Pro	Pro	Gly	Gly	Gly	Leu	Val	Phe	Glu	Leu	Trp
	355					360						365			
Gln	Asn	Pro	Asp	Asn	His	Gln	Arg	Tyr	Val	Ala	Val	Lys	Met	Phe	Tyr
	370					375					380				

Gln Thr Met Asp Gln Leu Arg Asn Ala Glu Lys Leu Asp Leu Lys Asn  
 385 390 395 400  
 Asn Pro Ala Gly Ile Ile Ser Val Ala Val Ala Gly Cys Glu Asn Asn  
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 Gly Asp Asp Lys Leu Cys Glu Leu Asp Thr Phe Gln Lys Lys Val Ala  
 420 425 430  
 Lys Val Ile Glu Pro Ala Cys His Ile  
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 <211> 1325  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetically generated

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 attttgagtc gccatgggtg tcgctcgccg accaaacaac gcagcttatg aatgatgtta 180  
 cgccagataa gtggccacaa tggccggtaa aagcggggta tttaacgcca cgtgggtgcg 240  
 agttgggtcac attgatgggg ggggttttatg gtgattactt tcgcagcctt ggtttggttag 300  
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 gcttaaccgg acaggcattt cttgatgggtg tggctccggg gtgtgggttg accgtgcata 420  
 atcaggccga tttgaaaaag accgatcccc tgttccatcc ggtagagact ggcgtgtgta 480  
 agttagacaa cgcacaaaaca gataaagcga ttgaagaacg attgggcggg ccgtagata 540  
 cggtgagcca gcgctacgct aaaccttttg ccagatggg ggacgtgctg aattttgcg 600  
 cttctcctta ttgcaaatct ttgcaacagc aaggaaaaac gtgtgatttt gccactttg 660  
 cggccaatga agttaacgtt aataaagaag ggacaaaagt gaccctcagt gggccactgg 720  
 cgttatcatc gacattgggt gaaatcttct tattacaaaa cgcacaagcc atgccagagg 780  
 ttgcctggca acggctaaaa ggggcggaga attgggtatc cttattgtca ttacataacg 840  
 cgcaatttaa tttaatggca aaaacaccgt atatcgcccc tcataaaggg acgccattat 900  
 tacagcagat agatacggct ttaacccttc aactggatgc tcaggggcaa aagctaccca 960  
 tttcagccca aaaccgggtc ttgttcctcg gtgggcatga taccaatatt gccaatattg 1020  
 cgggtatgct gggagccgac tggcagctac ccgagcaacc tgataaatac ccaccaggtg 1080  
 ggggattggg ttttgaacta tggcaaaatc cggataacca ccagcgctac gttgcggtga 1140  
 agatgttcta ccaaacgatg gatcagttgc gtaatgccga aaaattggat ctgaaaaata 1200  
 acccagcggg tattatttcc gttgcagttg ctggttggtg aaataacggt gacgataagc 1260  
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 <211> 420  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetically generated

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 Gly Tyr Thr Leu Glu Arg Val Val Ile Leu Ser Arg His Gly Val Arg  
 35 40 45

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65					70					75					80
Glu	Leu	Val	Thr	Leu	Met	Gly	Gly	Phe	Tyr	Gly	Asp	Tyr	Phe	Arg	Ser
				85					90					95	
Leu	Gly	Leu	Leu	Ala	Ala	Gly	Cys	Pro	Ala	Glu	Gly	Gly	Val	Tyr	Ala
			100					105					110		
Gln	Ala	Asp	Ile	Asp	Gln	Arg	Thr	Arg	Leu	Thr	Gly	Gln	Ala	Phe	Leu
		115					120					125			
Asp	Gly	Val	Ala	Pro	Gly	Cys	Gly	Leu	Thr	Val	His	Asn	Gln	Ala	Asp
	130					135					140				
Leu	Lys	Lys	Thr	Asp	Pro	Leu	Phe	His	Pro	Val	Glu	Thr	Gly	Val	Cys
145					150					155					160
Lys	Leu	Asp	Asn	Ala	Gln	Thr	Asp	Lys	Ala	Ile	Glu	Glu	Arg	Leu	Gly
				165					170					175	
Gly	Pro	Leu	Asp	Thr	Val	Ser	Gln	Arg	Tyr	Ala	Lys	Pro	Phe	Ala	Gln
			180					185					190		
Met	Gly	Asp	Val	Leu	Asn	Phe	Ala	Ala	Ser	Pro	Tyr	Cys	Lys	Ser	Leu
	195					200						205			
Gln	Gln	Gln	Gly	Lys	Thr	Cys	Asp	Phe	Ala	His	Phe	Ala	Ala	Asn	Glu
	210					215					220				
Val	Asn	Val	Asn	Lys	Glu	Gly	Thr	Lys	Val	Thr	Leu	Ser	Gly	Pro	Leu
225					230					235					240
Ala	Leu	Ser	Ser	Thr	Leu	Gly	Glu	Ile	Phe	Leu	Leu	Gln	Asn	Ala	Gln
				245					250					255	
Ala	Met	Pro	Glu	Val	Ala	Trp	Gln	Arg	Leu	Lys	Gly	Ala	Glu	Asn	Trp
			260					265					270		
Val	Ser	Leu	Leu	Ser	Leu	His	Asn	Ala	Gln	Phe	Asn	Leu	Met	Ala	Lys
	275						280					285			
Thr	Pro	Tyr	Ile	Ala	Arg	His	Lys	Gly	Thr	Pro	Leu	Leu	Gln	Gln	Ile
	290					295					300				
Asp	Thr	Ala	Leu	Thr	Leu	Gln	Leu	Asp	Ala	Gln	Gly	Gln	Lys	Leu	Pro
305					310					315					320
Ile	Ser	Ala	Gln	Asn	Arg	Val	Leu	Phe	Leu	Gly	Gly	His	Asp	Thr	Asn
				325					330					335	
Ile	Ala	Asn	Ile	Ala	Gly	Met	Leu	Gly	Ala	Asp	Trp	Gln	Leu	Pro	Glu
		340						345					350		
Gln	Pro	Asp	Asn	Thr	Pro	Pro	Gly	Gly	Gly	Leu	Val	Phe	Glu	Leu	Trp
		355					360					365			
Gln	Asn	Pro	Asp	Asn	His	Gln	Arg	Tyr	Val	Ala	Val	Lys	Met	Phe	Tyr
	370					375					380				
Gln	Thr	Met	Asp	Gln	Leu	Arg	Asn	Ala	Glu	Lys	Leu	Asp	Leu	Lys	Asn
385					390					395					400
Asn	Pro	Ala	Gly	Ile	Ile	Ser	Val	Ala	Val	Ala	Gly	Cys	Glu	Asn	Asn
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<210> 5

<211> 1266

<212> DNA

<213> Artificial Sequence

<220>

<223> 953-6 phytase sequence

<400> 5

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ccgggggtcgc taaagctcga aaaggtcgtg atgctgatgc gccacggcgt tcgcccgcga 180
accaaggcgg cgggtggtgcc gcccggttat tcggccgaaa catggcccga ctggccgggtc 240
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ctcgcgccagg cgcgcgaggg cgggctgacc gccgaaaccg cagcccatcg cggcgaactg 600
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<210> 6

<211> 421

<212> PRT

<213> Artificial Sequence

<220>

<223> 953-6 phytase sequence

<400> 6

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Gly Ala Asp Ala Ser Pro Ala Ala Pro Gly Ser Leu Lys Leu Glu Lys
          35          40          45
Val Val Met Leu Met Arg His Gly Val Arg Pro Pro Thr Lys Ala Ala
          50          55          60
Val Val Pro Pro Gly Tyr Ser Ala Glu Thr Trp Pro Asp Trp Pro Val
65          70          75          80
Asp Phe Gly Leu Leu Thr Pro His Gly Ala Ala Gly Val Lys Leu Leu
          85          90          95
Gly Glu Ser Asp Arg Leu Thr Phe Gly Gly Arg Gly Leu Phe Pro Asp
          100         105         110
Gly Cys Pro Ala Ala Gly Thr Ile Val Leu Lys Ala Ser Tyr Lys Glu
          115         120         125
Arg Thr Ile Ala Thr Ala Gln Asn Trp Ala Ala Gly Phe Met Pro Gly
130         135         140
Cys Thr Ala Asp Val Ala His Pro Ala Gly Pro Asp Asp Asp Ala Ile
145         150         155         160
Phe His Gly Leu Asp Gly Gly Pro Ala Ser Phe Asp Gly Lys Arg Ala
          165         170         175
Phe Asp Ala Ala Leu Ala Gln Ala Pro Glu Gly Gly Leu Thr Ala Glu
          180         185         190
Thr Ala Arg His Arg Gly Glu Leu Thr Leu Leu Ala Lys Val Leu Asn
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195	200	205
Cys Ala Leu Pro Ala Cys	Pro Leu Ile Ala Glu	Pro Ser Arg Leu Val
210	215	220
Ala Gln Pro His Asp Arg	Pro Asp Leu Glu Gly	Pro Leu Asp Val Gly
225	230	235
Ser Thr Ala Ser Gln Thr	Leu Val Leu Glu Tyr	Leu Glu Gly Lys Pro
245	250	255
Met Ala Glu Val Gly Trp	Gly Arg Val Ser Arg	Ala Glu Ile Glu Gln
260	265	270
Leu Leu Arg Phe His Pro	Leu Lys Phe Arg Tyr	Ser Asn Arg Pro Gly
275	280	285
Tyr Ile Ala Ala Ala Ala	Ala Pro Ile Val Arg	Glu Ile Val Ala
290	295	300
Ala Leu Asp Ser Asn Ser	Pro Ala Arg Leu Thr	Leu Leu Ala Gly His
305	310	315
Asp Thr Asn Val Ala Asp	Leu Gly Gly Phe Phe	Asp Leu His Trp Gln
325	330	335
Val Pro Ser Tyr Pro Ala	Asp Glu Val Pro Pro	Gly Ser Ala Leu Gly
340	345	350
Phe Glu Leu Val Ser Asn	Ala Lys Gly Asp Arg	Tyr Val Arg Ala Phe
355	360	365
Tyr Arg Ala Gln Thr Met	Asp Gln Leu Arg Asn	Leu Glu Pro Leu Gly
370	375	380
Ser Gly Asp Ala Leu Tyr	Arg Arg Tyr Leu Pro	Ile Pro Gly Cys Gly
385	390	395
His Ser Val Glu Ala Thr	Ala Cys Ser Trp Ser	Asp Phe Ala Arg Leu
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Ala Ala Pro Arg Gly		
420		

<210> 7  
 <211> 1230  
 <212> DNA  
 <213> Rhizobium

<400> 7

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gaaacatggc	ccgactggcc	ggtcgatttc	ggcctgctga	cgccgcacgc	cgcggcgggg	240
gtcaagcttc	tcggcgaaa	cgaccgcctc	tatttcggcg	gtcgcgccct	gtttcccag	300
ggatgcccgc	cggcgggcac	gatcgtcctc	aaggcgagct	acaaggagcg	cacgatcgcc	360
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gccggtccgc	acgatgacgc	gatctttcat	gggctcgacg	gcggccccgc	ctcgttcgac	480
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tttgaactgg	tcagcaatgc	gaagggcgac	cgctatgtcc	gcgccttcta	tcgcgggcag	1080
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tatcttccca	ttccgggggtg	cggcaattcg	gtcgaggcga	ccgcctgcgc	ctggagtgat	1200
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<210> 8  
 <211> 409  
 <212> PRT  
 <213> Rhizobium

<400> 8  
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 35 40 45  
 Thr Lys Ala Ala Val Val Pro Pro Gly Tyr Ser Ala Glu Thr Trp Pro  
 50 55 60  
 Asp Trp Pro Val Asp Phe Gly Leu Leu Thr Pro His Gly Ala Ala Gly  
 65 70 75 80  
 Val Lys Leu Leu Gly Glu Ser Asp Arg Leu Tyr Phe Gly Gly Arg Gly  
 85 90 95  
 Leu Phe Pro Glu Gly Cys Pro Ala Ala Gly Thr Ile Val Leu Lys Ala  
 100 105 110  
 Ser Tyr Lys Glu Arg Thr Ile Ala Thr Ala Gln Ser Trp Ala Ala Gly  
 115 120 125  
 Phe Met Pro Gly Cys Ala Thr Asp Val Ala His Pro Ala Gly Pro Asp  
 130 135 140  
 Asp Asp Ala Ile Phe His Gly Leu Asp Gly Gly Pro Ala Ser Phe Asp  
 145 150 155 160  
 Gly Lys Arg Ala Phe Asp Ala Ala Leu Ala Gln Ala Pro Glu Gly Gly  
 165 170 175  
 Leu Thr Ala Glu Thr Ala Arg His Arg Gly Glu Leu Thr Leu Leu Ala  
 180 185 190  
 Lys Val Leu Asn Cys Ala Leu Pro Ala Cys Pro Leu Ile Ala Glu Pro  
 195 200 205  
 Ser Arg Leu Val Ala Gln Pro His Asp Arg Pro Glu Ile Glu Gly Pro  
 210 215 220  
 Leu Asp Val Gly Ser Thr Ala Ser Gln Thr Leu Val Leu Glu Tyr Leu  
 225 230 235 240  
 Glu Gly Lys Pro Met Ala Glu Val Gly Trp Gly Arg Val Ser Arg Ala  
 245 250 255  
 Glu Ile Glu Gln Leu Leu Arg Phe His Pro Leu Lys Phe Arg Tyr Ser  
 260 265 270  
 Asn Arg Pro Gly Tyr Ile Ala Ala Thr Ala Ala Ala Pro Ile Val Arg  
 275 280 285  
 Glu Ile Val Thr Ala Leu Gly Asp Arg Ser Pro Ala Arg Leu Thr Leu  
 290 295 300  
 Leu Ala Gly His Asp Thr Asn Val Ala Asp Leu Gly Gly Phe Phe Asp  
 305 310 315 320  
 Leu His Trp Gln Val Pro Ser Tyr Pro Ala Asp Glu Val Pro Pro Gly  
 325 330 335  
 Ser Ala Leu Gly Phe Glu Leu Val Ser Asn Ala Lys Gly Asp Arg Tyr  
 340 345 350  
 Val Arg Ala Phe Tyr Arg Gly Gln Thr Met Asp Gln Leu Arg Asn Leu  
 355 360 365  
 Glu Pro Leu Arg Ser Asp Asp Thr Leu Phe Arg Arg Tyr Leu Pro Ile  
 370 375 380  
 Pro Gly Cys Gly Asn Ser Val Glu Ala Thr Ala Cys Ala Trp Ser Asp  
 385 390 395 400  
 Phe Ala Arg Leu Ala Ala Pro Arg Gly

<210> 9  
 <211> 1431  
 <212> DNA

<213> Artificial Sequence

<220>

<223> 954-2 phytase sequence

<400> 9

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atgaagaaga cgatatggag gagagttaga cagcgatggc gaaggggtgc gtgtgccgca 60
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gcgggtagcg agccgccccg gaaggccgcg gcaacagatg gcatgccgca agactggtcg 180
ctcgacgcgt tggtcacgtg cagccggcac ggcgtgcggt ctccgacgcg tccggagccg 240
ccgctggaga gcctcagccc cgatccgtgg ccccgatggc ccgtgccgac tgcccacctg 300
accgatcgtg gcgcgggcgt cgtctcgcag atggggcggt actacggtga ttggcttcgt 360
gcccgggggtg tgctgccggc cagcgggtgc cctgcgaccg gaacgcctta cggatgggca 420
gacgttgacc agcggacccg tctgacgggc gacgccctgc tcctcggcat ggcgccaggc 480
tgcggtatcc acagcgatca tcgcgcggcg ctcgacgaga aggatccgat cttccacgcg 540
atggaatcgg gtgcatgccc agtcgacccc gtacaggcga agcgcgacat cgaagcgcat 600
gccggcgagg gcggcgtggc gacactggga aggcgctacg cagcaagcct gaccagaatg 660
agcgaggtgc tcgactacgc ccatagcgcc gattgcgcga ggcattggcg ccaatgcgac 720
tatgcgcgcc aacccaatcg tgctcgagatc agaccagatg gccttcacgc cgcgttgaag 780
ggcccgatgg gcagtgttc gaccgtctcc gaggtcttcc tgctcgaaca tgggcagggc 840
ctgccacagg agcaggttgc atggggccgt atccacgatg cgcaggactg gacgtgtctg 900
atgcaggcgc ataacgcgca gttcgatctg atggcgaaga cgccttacat ggctactcga 960
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accgcgcatg acacgaatct tgcacacttg gccggcttgc tgcacttgga ctggaccctg 1140
cccagcaaac cggacgacac gccgcggggc ggtgcaatgg tgttctcctt gtggcgggag 1200
cctggcacgc aggcacgttt cgttcgcgtg gagatggtct atcagtcgat ggatcagctt 1260
cggcagctca cgcgctctc cctggcgcag ccgcccacgc gcctgatctt gccgttgccc 1320
ggctgtgccg acgcggcgca cggacatgca tgcagcctgc cggagttcag ccggcgtgtg 1380
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<210> 10

<211> 476

<212> PRT

<213> Artificial Sequence

<220>

<223> 954-2 phytase sequence

<400> 10

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Met Lys Lys Thr Ile Trp Arg Arg Val Gly Gln Arg Trp Arg Arg Gly
1      5      10      15
Ala Cys Ala Ala Thr Val Leu Leu Ser Ala Cys Ser Thr Gln Leu Pro
20     25     30
Gly Val Pro Ala Thr Leu Ser Ala Ala Gly Ser Glu Pro Pro Arg Lys
35     40     45
Ala Ala Ala Thr Asp Gly Met Pro Gln Asp Trp Ser Leu Asp Ala Leu
50     55     60
Val Ile Val Ser Arg His Gly Val Arg Ser Pro Thr Arg Pro Glu Pro
65     70     75     80
Pro Leu Glu Ser Leu Ser Pro Asp Pro Trp Pro Gln Trp Pro Val Pro
85     90     95

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Thr	Ala	His	Leu	Thr	Asp	Arg	Gly	Ala	Ala	Leu	Val	Ser	Gln	Met	Gly	
			100					105					110			
Arg	Tyr	Tyr	Gly	Asp	Trp	Leu	Arg	Ala	Arg	Gly	Val	Leu	Pro	Ala	Ser	
		115					120					125				
Gly	Cys	Pro	Ala	Thr	Gly	Thr	Leu	Tyr	Gly	Trp	Ala	Asp	Val	Asp	Gln	
	130					135					140					
Arg	Thr	Arg	Leu	Thr	Gly	Asp	Ala	Leu	Leu	Leu	Gly	Met	Ala	Pro	Gly	
145					150					155					160	
Cys	Gly	Ile	His	Ser	Asp	His	Arg	Ala	Ala	Leu	Asp	Glu	Lys	Asp	Pro	
			165					170						175		
Ile	Phe	His	Ala	Met	Glu	Ser	Gly	Ala	Cys	Pro	Val	Asp	Pro	Val	Gln	
		180					185						190			
Ala	Lys	Arg	Asp	Ile	Glu	Ala	His	Ala	Gly	Glu	Gly	Gly	Val	Ala	Thr	
	195					200					205					
Leu	Gly	Arg	Arg	Tyr	Ala	Ala	Ser	Leu	Thr	Arg	Met	Ser	Glu	Val	Leu	
	210				215					220						
Asp	Tyr	Ala	His	Ser	Ala	Asp	Cys	Ala	Arg	His	Gly	Gly	Gln	Cys	Asp	
225				230				235						240		
Tyr	Ala	Arg	Gln	Pro	Asn	Arg	Val	Glu	Ile	Arg	Pro	Asp	Gly	Leu	His	
			245					250					255			
Ala	Ala	Leu	Lys	Gly	Pro	Met	Gly	Ser	Ala	Ser	Thr	Val	Ser	Glu	Val	
		260					265						270			
Phe	Leu	Leu	Glu	His	Gly	Gln	Gly	Leu	Pro	Gln	Glu	Gln	Val	Ala	Trp	
	275					280						285				
Gly	Arg	Ile	His	Asp	Ala	Gln	Asp	Trp	Thr	Leu	Leu	Met	Gln	Ala	His	
	290				295					300						
Asn	Ala	Gln	Phe	Asp	Leu	Met	Ala	Lys	Thr	Pro	Tyr	Met	Ala	Thr	Arg	
305				310				315						320		
Arg	Gly	Thr	Pro	Met	Leu	Ala	Ser	Val	Leu	Asp	Ala	Leu	Glu	Arg	Arg	
			325					330					335			
Ala	Gly	Ala	Pro	Ala	Pro	Glu	Leu	Ala	Val	Lys	Gly	Pro	Lys	Leu	Pro	
		340					345					350				
Gln	Gly	Asn	Arg	Val	Tyr	Val	Leu	Thr	Ala	His	Asp	Thr	Asn	Leu	Ala	
	355					360					365					
His	Leu	Ala	Gly	Leu	Leu	His	Leu	Asp	Trp	Thr	Leu	Pro	Glu	Gln	Pro	
	370				375					380						
Asp	Asp	Thr	Pro	Pro	Gly	Gly	Ala	Met	Val	Phe	Ser	Leu	Trp	Arg	Glu	
385				390					395					400		
Pro	Gly	Thr	Gln	Ala	Arg	Phe	Val	Arg	Val	Glu	Met	Val	Tyr	Gln	Ser	
			405				410						415			
Met	Asp	Gln	Leu	Arg	Gln	Leu	Thr	Pro	Leu	Ser	Leu	Ala	Gln	Pro	Pro	
		420					425					430				
His	Arg	Leu	Ile	Leu	Pro	Leu	Pro	Gly	Cys	Ala	Asp	Ala	Ala	His	Gly	
	435					440					445					
His	Ala	Cys	Ser	Leu	Pro	Glu	Phe	Ser	Arg	Arg	Val	Arg	Ala	Ala	Leu	
	450				455					460						
Ser	Pro	Ser	Cys	Leu	Glu	Ala	Val	Thr	Ala	Ala	His					
465				470				475								

<210> 11

<211> 1326

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetically generated

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<400> 11
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atthttgagtc gccatggtgt gcgtagcccg actaagcaga cgcagctgat gaatgatgta 180
acacctgata agtggcctca gtggccgggt aaagcggggc atttgactcc tcgtggcgcc 240
gaactgggtca ccctgatggg cgggttctat ggcgattatt tccgcagttt gggctctttg 300
gccgcgggct gcccggcaga gggcggtgta tatgcacagg cagatatcga ccagcgcact 360
cgthtaaccg gtcaggcttt tctggatggt gtggcgccgg gttgcggcct gactgtccac 420
aatcaggccg atcttaagaa aaccgatcct ctgtttcatc ccgttgaaac cggcgtctgt 480

aaactggaca acgccc aaac cgataaggca attgaggaac gcctggggcgg cccgttagac 540
acggtaagcc agcgctatgc caaacggtt gcgcaaattg gcgatgtcct gaacttcgct 600
gcgagtcctg actgcaagtc actgcagcag caggggaaaa cttgtgactt cgcacacttt 660
gcggccaaac aggttaatgt aaacaaggaa ggcacgaaag ttaccctgtc agggccccctg 720
gcgctgtcta atcggttggg cgaaatcttc ttgctgcaga acgcgcaggc gatgccgaa 780
gtagcgtggc agcgtttgaa aggcgtgag aactgggtgt ctcttctgag cctgcacaat 840
gcacagttca acctgatggc taaaacgcca tacattgcac gccacaaagg cagccgctt 900
ttacagcaaa tcgataccgc actgaccctg caactggacg cccaggggca aaaactgccg 960
atctcggctc agaaccgtgt tttattcctg ggtggccacg acacaaatat tgctaacatc 1020
gccggtatgc tgggcgcaga ttggcagtta ccggaacaac cggataaacac cccaccgggc 1080
ggcgggtctg tctttgagct gtggcagaat ccggacaatc atcaacgtta tgtggccgtt 1140
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aatcccgccg gcatcatcag tgtcgtgtg gccggctgcg agaataatgg tgacgataaa 1260
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atttaa 1326

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<210> 12
<211> 441
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetically generated

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<400> 12
Met Ser Gly Leu Glu Asn Arg Val Arg Leu Ser Gly Leu Val Leu Met
1 5 10 15
Leu Ser Gly Leu Ala Ala Ile Thr Ala Pro Val Ala Ala Glu Pro Ser
20 25 30
Gly Tyr Thr Leu Glu Arg Val Val Ile Leu Ser Arg His Gly Val Arg
35 40 45
Ser Pro Thr Lys Gln Thr Gln Leu Met Asn Asp Val Thr Pro Asp Lys
50 55 60
Trp Pro Gln Trp Pro Val Lys Ala Gly Tyr Leu Thr Pro Arg Gly Ala
65 70 75 80
Glu Leu Val Thr Leu Met Gly Gly Phe Tyr Gly Asp Tyr Phe Arg Ser
85 90 95
Leu Gly Leu Leu Ala Ala Gly Cys Pro Ala Glu Gly Gly Val Tyr Ala
100 105 110
Gln Ala Asp Ile Asp Gln Arg Thr Arg Leu Thr Gly Gln Ala Phe Leu
115 120 125
Asp Gly Val Ala Pro Gly Cys Gly Leu Thr Val His Asn Gln Ala Asp
130 135 140
Leu Lys Lys Thr Asp Pro Leu Phe His Pro Val Glu Thr Gly Val Cys
145 150 155 160
Lys Leu Asp Asn Ala Gln Thr Asp Lys Ala Ile Glu Glu Arg Leu Gly
165 170 175
Gly Pro Leu Asp Thr Val Ser Gln Arg Tyr Ala Lys Pro Phe Ala Gln
180 185 190

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Met Gly Asp Val Leu Asn Phe Ala Ala Ser Pro Tyr Cys Lys Ser Leu  
 195 200 205  
 Gln Gln Gln Gly Lys Thr Cys Asp Phe Ala His Phe Ala Ala Asn Glu  
 210 215 220  
 Val Asn Val Asn Lys Glu Gly Thr Lys Val Thr Leu Ser Gly Pro Leu  
 225 230 235 240  
 Ala Leu Ser Ser Thr Leu Gly Glu Ile Phe Leu Leu Gln Asn Ala Gln  
 245 250 255  
 Ala Met Pro Glu Val Ala Trp Gln Arg Leu Lys Gly Ala Glu Asn Trp  
 260 265 270  
 Val Ser Leu Leu Ser Leu His Asn Ala Gln Phe Asn Leu Met Ala Lys  
 275 280 285  
  
 Thr Pro Tyr Ile Ala Arg His Lys Gly Thr Pro Leu Leu Gln Gln Ile  
 290 295 300  
 Asp Thr Ala Leu Thr Leu Gln Leu Asp Ala Gln Gly Gln Lys Leu Pro  
 305 310 315 320  
 Ile Ser Ala Gln Asn Arg Val Leu Phe Leu Gly Gly His Asp Thr Asn  
 325 330 335  
 Ile Ala Asn Ile Ala Gly Met Leu Gly Ala Asp Trp Gln Leu Pro Glu  
 340 345 350  
 Gln Pro Asp Asn Thr Pro Pro Gly Gly Gly Leu Val Phe Glu Leu Trp  
 355 360 365  
 Gln Asn Pro Asp Asn His Gln Arg Tyr Val Ala Val Lys Met Phe Tyr  
 370 375 380  
 Gln Thr Met Asp Gln Leu Arg Asn Ala Glu Lys Leu Asp Leu Lys Asn  
 385 390 395 400  
 Asn Pro Ala Gly Ile Ile Ser Val Ala Val Ala Gly Cys Glu Asn Asn  
 405 410 415  
 Gly Asp Asp Lys Leu Cys Glu Leu Asp Thr Phe Gln Lys Lys Val Ala  
 420 425 430  
 Lys Val Ile Glu Pro Ala Cys His Ile  
 435 440

<210> 13  
 <211> 410  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> amino acid sequence of a phytase enzyme with  
 predicted glycosylation sites

<400> 13  
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 1 5 10 15  
 His Gly Val Arg Ala Pro Thr Lys Ala Thr Gln Leu Met Gln Asp Val  
 20 25 30  
 Thr Pro Asp Ala Trp Pro Thr Trp Pro Val Lys Leu Gly Glu Leu Thr  
 35 40 45  
 Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu Gly His Tyr Trp Arg Gln  
 50 55 60  
 Arg Leu Val Ala Asp Gly Leu Leu Pro Lys Cys Gly Cys Pro Gln Ser  
 65 70 75 80  
 Gly Gln Val Ala Ile Ile Ala Asp Val Asp Glu Arg Thr Arg Lys Thr  
 85 90 95  
 Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro Asp Cys Ala Ile Thr Val  
 100 105 110



65					70					75				80	
Ala	Ala	Gly	Thr	Ile	Leu	Ala	Asp	Val	Asp	Glu	Arg	Thr	Arg	Thr	Gly
				85					90					95	
Gln	Ala	Phe	Ala	Ala	Gly	Leu	Ala	Pro	Gly	Cys	Ala	Ile	Val	His	Ala
			100					105					110		
Gly	Asp	Asp	Pro	Ile	Phe	His	Gly	Leu	Asp	Thr	Gly	Cys	Leu	Asp	Gln
		115					120					125			
Ala	Asp	Ala	Ile	Leu	Ala	Ala	Gly	Glu	Gly	Gly	Leu	Thr	Ala	Arg	His
	130					135					140				
Gly	Leu	Thr	Leu	Ala	Lys	Val	Leu	Asn	Phe	Ala	Ser	Ala	Cys	Leu	Glu
145					150					155					160
Cys	Ala	Arg	Val	Val	Gly	Arg	Leu	Gly	Pro	Leu	Leu	Ala	Ser	Thr	Leu

  

				165					170					175	
Ser	Glu	Ile	Phe	Leu	Leu	Glu	Tyr	Ala	Gln	Gly	Pro	Met	Glu	Val	Gly
			180					185					190		
Trp	Gly	Arg	Ile	Ser	Ala	Glu	Trp	Leu	Leu	His	Asn	Ala	Gln	Phe	Leu
		195					200					205			
Met	Asn	Arg	Thr	Pro	Tyr	Ile	Ala	Arg	Ala	Thr	Pro	Ile	Leu	Ile	Val
	210					215					220				
Thr	Ala	Leu	Ser	Pro	Ala	Arg	Val	Val	Leu	Leu	Ala	Gly	His	Asp	Thr
225					230					235					240
Asn	Leu	Ala	Leu	Gly	Gly	Leu	Asp	Leu	Trp	Gln	Leu	Pro	Gln	Pro	Asp
				245					250					255	
Glu	Thr	Pro	Pro	Gly	Gly	Ala	Leu	Val	Phe	Glu	Leu	Trp	Asn	Arg	Tyr
			260					265					270		
Val	Arg	Val	Met	Tyr	Gln	Thr	Met	Asp	Gln	Leu	Arg	Asn	Leu	Glu	Pro
	275						280					285			
Leu	Leu	Pro	Arg	Ile	Leu	Pro	Ile	Pro	Gly	Cys	Gly	Ser	Glu	Ala	Ala
	290					295					300				
Cys	Ser	Leu	Ser	Asp	Phe	Ala	Arg	Leu	Val	Ala	Pro	Ala	Cys		
305					310					315					

<210> 15

<211> 410

<212> PRT

<213> Artificial Sequence

<220>

<223> amino acid sequence of a phytase enzyme with  
predicted glycosylation sites

<400> 15

Gln	Ser	Glu	Pro	Glu	Leu	Lys	Leu	Glu	Ser	Val	Val	Ile	Val	Ser	Arg
1				5				10					15		
His	Gly	Val	Arg	Ala	Pro	Thr	Lys	Ala	Thr	Gln	Leu	Met	Gln	Asp	Val
			20					25					30		
Thr	Pro	Asp	Ala	Trp	Pro	Thr	Trp	Pro	Val	Lys	Leu	Gly	Glu	Leu	Thr
		35					40					45			
Pro	Arg	Gly	Gly	Glu	Leu	Ile	Ala	Tyr	Leu	Gly	His	Tyr	Trp	Arg	Gln
	50					55				60					
Arg	Leu	Val	Ala	Asp	Gly	Leu	Leu	Pro	Lys	Cys	Gly	Cys	Pro	Gln	Ser
65					70				75						80
Gly	Gln	Val	Ala	Ile	Ile	Ala	Asp	Val	Asp	Glu	Arg	Thr	Arg	Lys	Thr
			85						90					95	
Gly	Glu	Ala	Phe	Ala	Ala	Gly	Leu	Ala	Pro	Asp	Cys	Ala	Ile	Thr	Val
		100						105					110		
His	Thr	Gln	Ala	Asp	Thr	Ser	Ser	Pro	Asp	Pro	Leu	Phe	Asn	Pro	Leu



Gly	His	Tyr	Gln	Arg	Gln	Arg	Leu	Val	Ala	Asp	Gly	Leu	Leu	Ala	Lys	
				85					90					95		
Lys	Gly	Cys	Pro	Gln	Ser	Gly	Gln	Val	Ala	Ile	Ile	Ala	Asp	Val	Asp	
			100					105					110			
Glu	Lys	Thr	Arg	Lys	Thr	Gly	Glu	Ala	Phe	Ala	Ala	Gly	Leu	Ala	Pro	
		115					120					125				
Asp	Cys	Ala	Ile	Thr	Val	His	Thr	Gln	Ala	Asp	Thr	Ser	Ser	Pro	Gly	
	130					135					140					
Pro	Leu	Phe	Asn	Pro	Leu	Lys	Thr	Gly	Val	Cys	Gln	Leu	Asp	Asn	Ala	
145					150					155					160	
Asn	Val	Thr	Asp	Ala	Ile	Leu	Ser	Arg	Ala	Gly	Gly	Ser	Ile	Ala	Asp	
			165						170						175	
Phe	Thr	Gly	His	Arg	Gln	Thr	Ala	Phe	Arg	Glu	Leu	Glu	Arg	Val	Leu	
			180					185					190			
Asn	Phe	Pro	Gln	Ser	Asn	Leu	Cys	Leu	Lys	Arg	Glu	Lys	Gln	Asp	Glu	
		195					200					205				
Ser	Cys	Ser	Leu	Thr	Gln	Ala	Leu	Pro	Ser	Glu	Leu	Lys	Val	Ser	Ala	
	210				215						220					
Asp	Asn	Val	Ser	Leu	Thr	Gly	Ala	Val	Ser	Leu	Ala	Ser	Met	Leu	Thr	
225				230						235					240	
Glu	Ile	Phe	Leu	Leu	Gln	Gln	Ala	Gln	Gly	Met	Pro	Glu	Pro	Gly	Trp	
			245					250						255		
Gly	Lys	Ile	Thr	Asp	Ser	His	Gln	Trp	Asn	Thr	Leu	Leu	Ser	Leu	Leu	
			260					265					270			
Asn	Ala	Gln	Phe	Tyr	Leu	Leu	Gln	Arg	Thr	Pro	Glu	Val	Ala	Arg	Ser	
	275						280					285				
Arg	Ala	Thr	Pro	Leu	Leu	Asp	Leu	Ile	Lys	Thr	Ala	Leu	Thr	Pro	His	
	290					295					300					
Pro	Pro	Gln	Lys	Gln	Ala	Tyr	Gly	Val	Thr	Leu	Pro	Thr	Ser	Val	Leu	
305				310						315					320	
Phe	Ile	Ala	Gly	His	Asp	Thr	Trp	Leu	Ala	Asn	Leu	Gly	Gly	Ala	Leu	
			325					330						335		
Glu	Leu	Asn	Trp	Thr	Leu	Pro	Gly	Gln	Pro	Asp	Asn	Thr	Pro	Pro	Gly	
		340					345						350			
Gly	Glu	Leu	Val	Phe	Glu	Arg	Trp	Arg	Arg	Leu	Ser	Asp	Asn	Ser	Gln	
	355						360					365				
Trp	Ile	Gln	Val	Ser	Leu	Val	Phe	Gln	Thr	Leu	Gln	Gln	Met	Asp	Asp	
	370					375					380					
Lys	Thr	Pro	Leu	Ser	Leu	Asn	Thr	Pro	Pro	Gly	Glu	Val	Lys	Leu	Thr	
385					390					395					400	
Leu	Ala	Gly	Cys	Glu	Glu	Arg	Asn	Ala	Gln	Gly	Met	Gln	Ser	Leu	Ala	
			405						410					415		
Gly	Phe	Thr	Gln	Ile	Val	Asn	Glu	Ala	Arg	Ile	Pro	Ala	Cys	Ser	Leu	
			420					425					430			

<210> 17

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> first region of a phytate sequence

<220>

<221> VARIANT

<222> 6

<223> Xaa = Any Amino Acid

<400> 17  
Arg His Gly Val Arg Xaa Pro Thr  
1 5

<210> 18  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> second region of a phytate sequence

<220>  
<221> VARIANT  
<222> 3  
<223> Xaa = Any Amino Acid

<400> 18  
Trp Pro Xaa Trp Pro Val  
1 5

<210> 19  
<211> 53  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide for the construction of Yersinia  
pestis phytase

<400> 19  
cttctactag aattcattaa agaggagaaa ttaaccatgt ccgtactgga gaa 53

<210> 20  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide for the construction of Yersinia  
pestis phytase

<400> 20  
ccgcgtccgc ctttccggtt tagtgtaa gctgtccggc ctggctgc 48

<210> 21  
<211> 53  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide for the construction of Yersinia  
pestis phytase

<400> 21



tatcacccgcg cctgtggccg ccgaaccatc ggggtacacc ttagaacgtg tag 53

<210> 22  
 <211> 55  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide for the construction of Yersinia  
 pestis phytase

<400> 22  
 ttattttgag tcgccatggt gtgcgtagcc cgactaagca gacgcagctg atgaa 55

<210> 23  
 <211> 64  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide for the construction of Yersinia  
 pestis phytase

<400> 23  
 tgatgtaaca cctgataagt ggcctcagtg gccgggtaaa gcgggctatt tgactcctcg 60  
 tggc 64

<210> 24  
 <211> 67  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide for the construction of Yersinia  
 pestis phytase

<400> 24  
 gccgaactgg tcaccctgat gggcggggttc tatggcgatt atttccgcag tttgggtctt 60  
 ttggccg 67

<210> 25  
 <211> 56  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide for the construction of Yersinia  
 pestis phytase

<400> 25  
 gccgcgggct gcccggcaga gggcggtgta tatgcacagg cagatatcga ccagcg 56

<210> 26  
 <211> 55  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> oligonucleotide for the construction of Yersinia  
pestis phytase

<400> 26  
cactcggttta accggtcagg cttttctgga tgggtgtggcg ccggggttgcg gcctg 55

<210> 27  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide for the construction of Yersinia  
pestis phytase

<400> 27  
actgtccaca atcaggccga tcttaagaaa accgatcctc tgtttcatcc 50

<210> 28  
<211> 54  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide for the construction of Yersinia  
pestis phytase

<400> 28  
cggttgaaacc ggcgtctgta aactggacaa cgcccaaacc gataaggcaa ttga 54

<210> 29  
<211> 58  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide for the construction of Yersinia  
pestis phytase

<400> 29  
ggaacgcctg ggcggcccgtagacacggt aagccagcgc tatgccaaac cgtttgcg 58

<210> 30  
<211> 67  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide for the construction of Yersinia  
pestis phytase

<400> 30  
caaattgggag atgtcctgaa cttcgctgag agtccgtact gcaagtcact gcagcagcag 60  
gggaaaa 67

<210> 31  
<211> 55  
<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide for the construction of Yersinia  
pestis phytase

<400> 31

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<211> 58

<212> DNA

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pestis phytase

<400> 32

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<210> 33

<211> 58

<212> DNA

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pestis phytase

<400> 33

cttgctgcag aacgcgcagg cgatgcccgga agtagcgtgg cagcgtttga aaggcgct 58

<210> 34

<211> 58

<212> DNA

<213> Artificial Sequence

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pestis phytase

<400> 34

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<210> 35

<211> 60

<212> DNA

<213> Artificial Sequence

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pestis phytase

<400> 35

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<210> 36  
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<210> 38  
 <211> 59  
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         pestis phytase

<400> 38  
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<210> 39  
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         pestis phytase

<400> 39  
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<210> 40  
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         pestis phytase

<400> 40  
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<210> 41  
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 pestis phytase

<400> 41  
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<210> 42  
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 pestis phytase

<400> 42  
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 ctacta 66

<210> 43  
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<220>  
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<400> 43  
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<210> 44  
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<400> 44  
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<210> 45  
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<210> 46  
<211> 53  
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pestis phytase

<400> 46  
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<210> 47  
<211> 54  
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<220>  
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pestis phytase

<400> 47  
acatcattca tcagctgcgt ctgcttagtc gggctacgca caccatggcg actc 54

<210> 48  
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pestis phytase

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tt 62

<210> 49  
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pestis phytase

<400> 49  
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gtt 63

<210> 50  
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<212> DNA  
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 pestis phytase

<400> 50  
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<210> 51  
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<220>  
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 pestis phytase

<400> 51  
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<210> 52  
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<400> 52  
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<210> 53  
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<220>  
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<400> 53  
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<210> 54  
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<220>  
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<400> 54  
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<210> 55  
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 <210> 56  
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 <210> 57  
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 <400> 57  
 agcaagaaga tttcgcccaa cgtgctagac agcgccaggg ggcctgacag ggtaactt 58  
  
 <210> 58  
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         pestis phytase  
  
 <400> 58  
 gttctcagcg cctttcaaac gctgccacgc tacttcgggc atcgctgcg cgttctgc 58  
  
 <210> 59  
 <211> 58  
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pestis phytase

<400> 59  
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<210> 60  
<211> 60  
<212> DNA  
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<220>  
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pestis phytase

<400> 60  
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<210> 61  
<211> 63  
<212> DNA  
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pestis phytase

<400> 61  
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gtt 63

<210> 62  
<211> 67  
<212> DNA  
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<220>  
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pestis phytase

<400> 62  
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ggccacc 67

<210> 63  
<211> 59  
<212> DNA  
<213> Artificial Sequence

<220>  
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pestis phytase

<400> 63  
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<210> 64  
<211> 55  
<212> DNA

<213> Artificial Sequence

<220>

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pestis phytase

<400> 64  
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<210> 65

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide for the construction of Yersinia  
pestis phytase

<400> 65  
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<210> 66

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

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pestis phytase

<400> 66  
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<210> 67

<211> 60

<212> DNA

<213> Artificial Sequence

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<400> 67  
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<210> 68

<211> 24

<212> DNA

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<220>

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<400> 68  
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<210> 69

<211> 35  
 <212> DNA  
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 <400> 69  
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 <210> 72  
 <211> 35  
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 <400> 72  
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 <210> 73  
 <211> 35  
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 <223> primer  
  
 <400> 73  
 tactgacgtc tcacaccag gaataaaaca cggtt 35  
  
 <210> 74  
 <211> 35  
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<220>

<223> primer

<400> 74

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35